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1 .....GCGA 4  
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50  
5 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 54  
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100  
55 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 104  
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 150  
105 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 154  
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 200  
155 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 204  
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250  
205 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 254  
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300  
255 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 304  
301 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350  
305 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 354  
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400  
355 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 404  
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450  
405 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 454  
451 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 500  
455 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 504  
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
505 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 554  
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
555 GATCAACGAAAACGCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 604  
601 GATCAACGAAAACGCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 1A

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605 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 654  
|||||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700  
  
655 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 704  
|||||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
  
705 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 754  
|||||  
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 800  
  
755 TGGCCAAAGATCGGATCACAGCCCTGTGATCAGTATCATGGCACGGCA 804  
|||||  
801 TGGCCAAAGATCGGATCACAGCCCTGTGATCAGTATCATGGCACGGCA 850  
  
805 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 854  
|||||  
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
  
855 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 904  
|||||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950  
  
905 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTATGGG 954  
|||||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTATGGG 1000  
  
955 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1004  
|||||  
1001 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1050  
  
1005 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTCCGGCTGCTGC 1054  
|||||  
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTCCGGCTGCTGC 1100  
  
1055 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1104  
|||||  
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150  
  
1105 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1154  
|||||  
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200  
  
1155 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1204  
|||||  
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1250  
  
1205 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1254  
|||||  
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig 1B

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1255 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1304  
|||||  
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350  
|||||  
1305 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1354  
|||||  
1351 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400  
|||||  
1355 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCAC 1404  
|||||  
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCA 1447  
|||||  
1405 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1454  
|||||  
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497  
|||||  
1455 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1504  
|||||  
1498 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547  
|||||  
1505 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1554  
|||||  
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597  
|||||  
1555 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1604  
|||||  
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1647  
|||||  
1605 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1654  
|||||  
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697  
|||||  
1655 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1704  
|||||  
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747  
|||||  
1705 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1754  
|||||  
1748 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797  
|||||  
1755 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1804  
|||||  
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847  
|||||  
1805 AAAG..... 1808  
|||||  
1848 AAAGCCCCGAG 1858

Fig. 1C

[illegible]

Fig. 2A

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636 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 685  
|||||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700  
686 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 735  
|||||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
736 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 785  
|||||  
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800  
786 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 835  
|||||  
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850  
836 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 885  
|||||  
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
886 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCC GTGATCGGGCGGTAA 935  
|||||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCC GTGATCGGGCGGTAA 950  
936 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 985  
|||||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000  
986 ATGAGTCCCGCCGATTTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1035  
|||||  
1001 ATGAGTCCCGCCGATTTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1050  
1036 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTGCGCTGCTGC 1085  
|||||  
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTGCGCTGCTGC 1100  
1086 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1135  
|||||  
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150  
1136 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1185  
|||||  
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200  
1186 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTTAAACATGATCG 1235  
|||||  
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTTAAACATGATCG 1250  
1236 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1285  
|||||  
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig. 2B

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1286 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1335  
|||||  
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350  
|||||  
1336 GCGTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1385  
|||||  
1351 GCGTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400  
|||||  
1386 GCGCGGACCTTATCCTGCTTGACCTGCGTCACCTCAGACGACTCCTCAC 1435  
|||||  
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACCTCAGACGACTCTCA 1447  
|||||  
1436 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1485  
|||||  
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497  
|||||  
1486 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1535  
|||||  
1498 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547  
|||||  
1536 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1585  
|||||  
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597  
|||||  
1586 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1635  
|||||  
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1647  
|||||  
1636 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1685  
|||||  
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697  
|||||  
1686 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1735  
|||||  
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747  
|||||  
1736 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1785  
|||||  
1748 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797  
|||||  
1786 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1835  
|||||  
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847  
|||||  
1836 AAAGGCCCCGAG 1846  
|||||  
1848 AAAGGCCCCGAG 1858

Fig. 2C

Fig. 3

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```

1  . . . . . SAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTG 45
   |||||||||||||||||||||||||||||||||||||||||||||||||||
1 SGNFLSAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTG 50

46 GMTTQLRCRFFDGVISALRRVTHYWRHIMQTLSIQHGTGLVTMDQYRRVLG 95
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
51 GMTTQLRCRFFDGVISALRRVTHYWRHIMQTLSIQHGTGLVTMDQYRRVLG 100
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
   . START .
96 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 145
   |||||||||||||||||||||||||||||||||||||||||||||||||||
101 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 150

146 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 195
   |||||||||||||||||||||||||||||||||||||||||||||||||||
151 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 200

196 INENADSAIYPGNIEAAMAVYGEVGVVVYARMFFDRMDGRIQGYVDALK 245
   |||||||||||||||||||||||||||||||||||||||||||||||||||
201 INENADSAIYPGNIEAAMAVYGEVGVVVYARMFFDRMDGRIQGYVDALK 250

246 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 295
   |||||||||||||||||||||||||||||||||||||||||||||||||||
251 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 300

296 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 345
   ||||||||||||||||||||||||||||||||||||||||:|||||||||
301 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 350

346 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSVAPVPPEMVERGMAV 395
   |||||||||||||||||||||||||||||||||||||||||||||||||||
351 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSVAPVPPEMVERGMAV 400

396 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 445
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
401 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 450

446 RSLGMDHEIGSIETGKRADLILLDLRHLPQTTPHHHLAATIVFQAYGNEVD 495
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
451 RSLGMDHEIGSIETGKRADLILLDLRHLLRRLS.HHLAATIVFQAYGNEVD 499

496 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 545
   |||||||||||||||||||||||||||||||||||||||||||||||||||
500 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 549
   STOP
546 SIQEMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 595
   |||||||||||||||||||||||||||||||||||||||||||||||||||
550 SIQEMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 599

596 SLVGEGRRLRAPASRRSERPE 615
   |||||||||||||:|||||
600 SLVGEGRRLRAPASRRGERPE 619

```

Fig. 4



*Fig. 5A*

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1 ...CCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 47  
|||  
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500  
G  
48 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 97  
|||  
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
98 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 147  
|||  
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
G  
148 GATCAACGAAAACNCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 197  
|||  
601 GATCAACGAAAACGCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 650  
198 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 247  
|||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700  
248 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 297  
|||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
G G  
298 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGANGAAACNGCTG 347  
|||  
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800  
G G G G  
348 TGGCCAAAGATCGGATCACANCCCTGT CANATCANTATCATGGCACNGCA 397  
|||  
801 TGGCCAAAGATCGGATCACAGCCCTGT CAGATCAGTATCATGGCACGGCA 850  
G G G  
398 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 447  
: |||  
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
448 ATTTAAANGAATCCATGGGCCA...ACCTCCCCCGTGATCCGGCGGTAA 493  
|||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCCGGCGGTAA 950  
494 TGTGAC..... 499  
|||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000

Fig. 5B

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360 .....TNGCAGGTTGTGAGCA..TGCTACTTC 336  
|:|||||||||||||||  
1101 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1150  
335 GGTTTCAGGNGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 286  
|||:|||||||||||||||||||||||||||||||||||||  
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200  
285 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 236  
|||||||||||||||||||||||||||||||||||||  
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGCAAACATGATCG 1250  
235 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 186  
|||||||||||||||||||||||||||||||||||||  
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300  
185 GACGTGCTGACCCCAGAGAAGATTNTTGAAATGGCGACGATCGATGGGGC 136  
|||||||||||||||||||||:|||||||||||||||||  
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350  
135 GCGTTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 86  
||| ||||||||||| |||||||||||||||||||  
1351 GCG.TTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 1399  
85 CGCGCGGACCTTATCCTGCTTGACCTGCGTCACCCTCAGACGACTCCTCA 36  
||||||||||||||||||||| |||||||||||  
1400 CGCGCGGACCTTATCCTGCTTGACCTGCGTCA.CCTCAGACGACTC..TC 1446  
35 CCATCATTTGGCGGCCACGATCGTGTTTCAGGCTT..... 1  
|||||||||||||||||  
1447 ACATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGG 1496  
.  
.  
.

Fig. 5C

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1 . . . . . CGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGACAC 43  
 |||||  
 1451 CATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGACAC 1500  
 44 TGTCTTGATTGACGGAAACGTTGTGATGGAGAACC GCCGCTTGAGCTTTC 93  
 |||||  
 1501 TGTCTTGATTGACGGAAACGTTGTGATGGAGAACC GCCGCTTGAGCTTTC 1550  
 94 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 143  
 |||||  
 1551 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 1600  
 144 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 193  
 |||||  
 1601 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 1649  
 194 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 243  
 |||||  
 1650 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 1699  
 244 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 293  
 |||||  
 1700 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 1749  
 294 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 343  
 |||||  
 1750 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 1799  
 344 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 393  
 |||||  
 1800 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 1849  
 394 AGCCCGAGGATCCTCTAGAGTCCGATTTTCCGATGTCATCACCGGCGCG 443  
 |||||  
 1850 AGGCCCCGAG . . . . . 1858

*Fig. 5D*

Fig. 6

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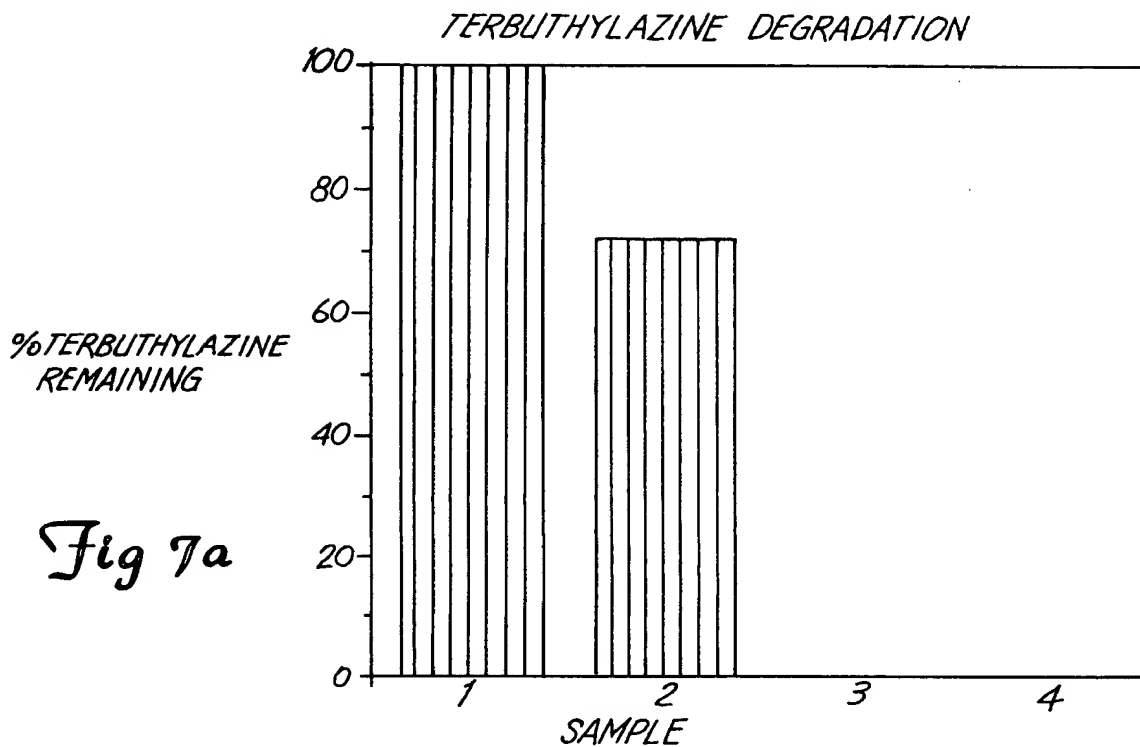


Fig 7a

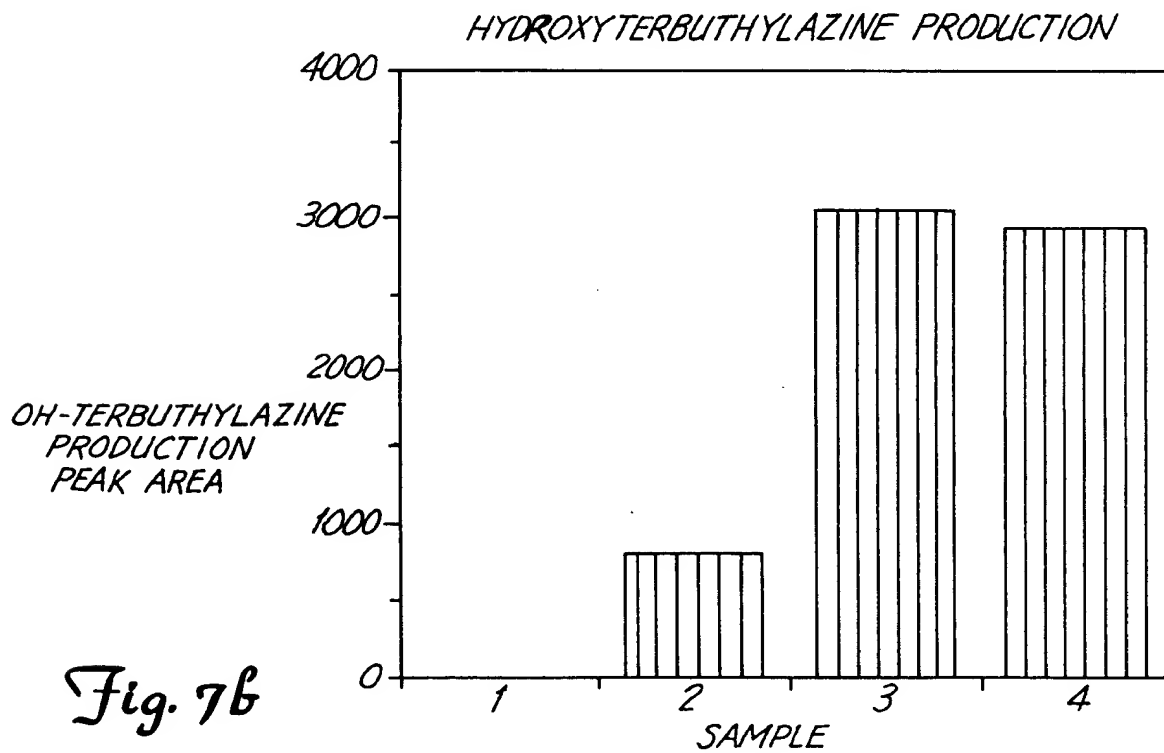
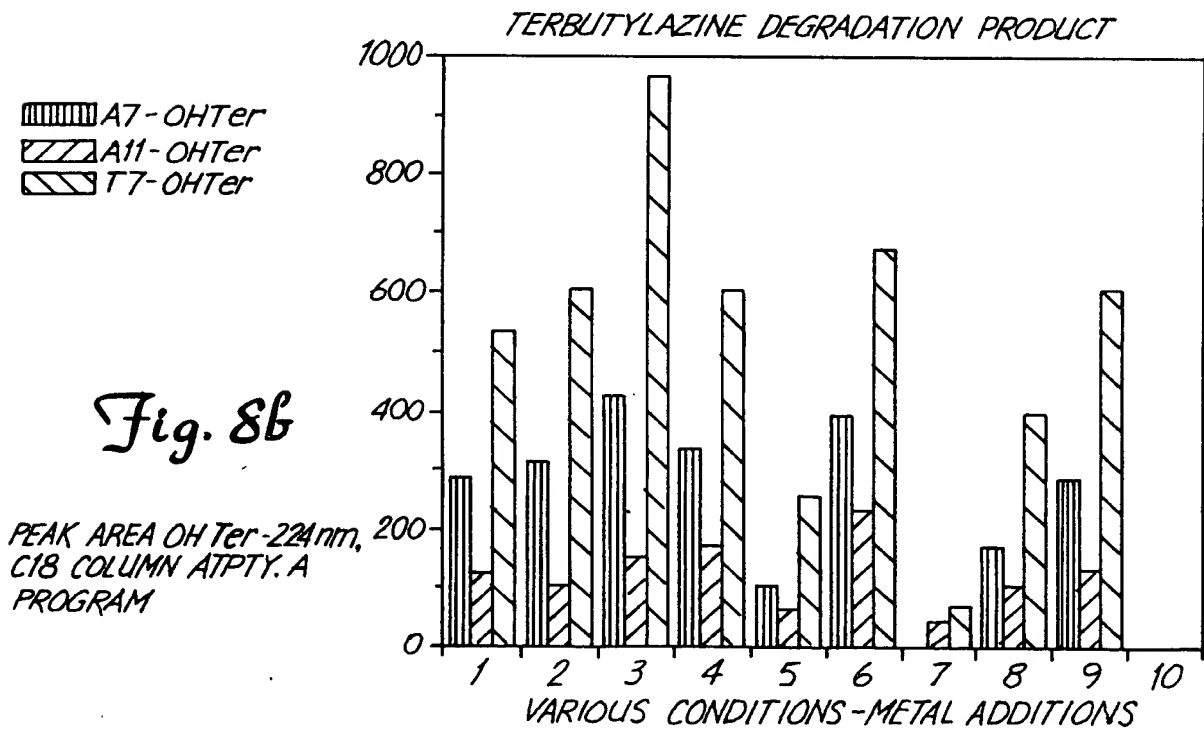
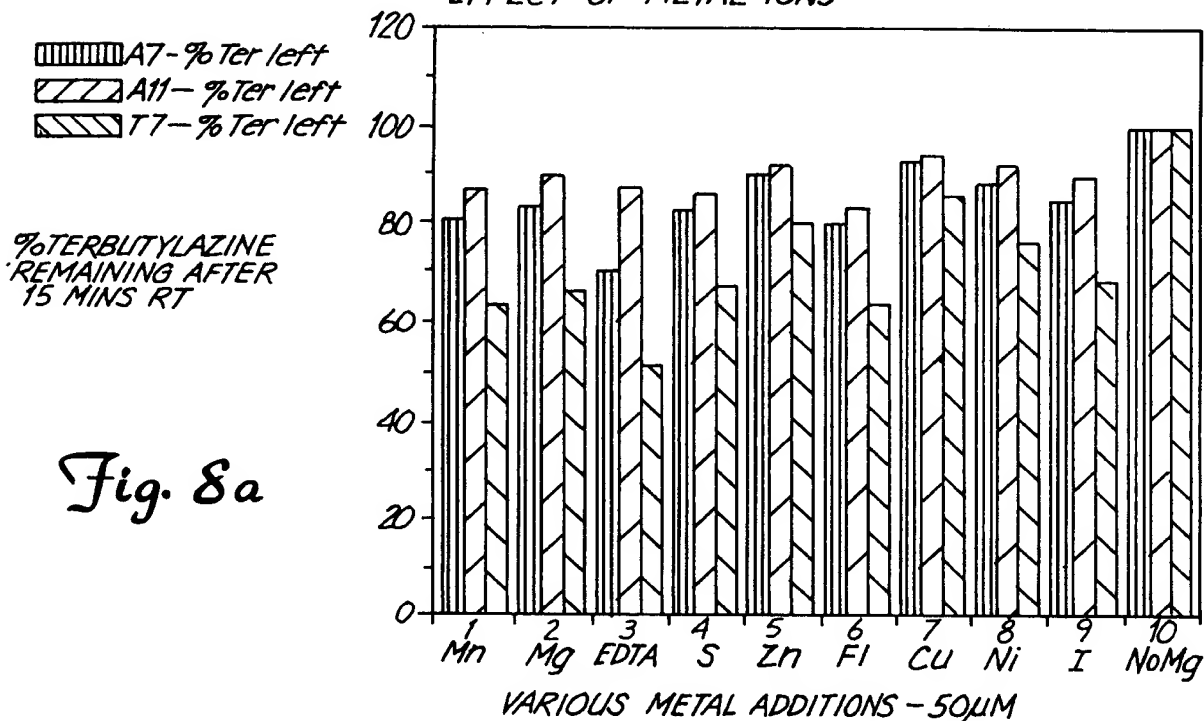


Fig. 7b

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TERBUTYLAZINE DEGRADATION BY SHUFFLED PROTEINS  
A7, A11 AND T7 - 1µg/ml ptn conc  
- EFFECT OF METAL IONS



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Bacterium      Translation of PCR amplified DNA sequence

		79	92		
ADP		SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
SG1		PHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
M91-3		SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
J14a		PHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
38/38		SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
Clav.		SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
		125			170
ADP	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
SG1	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
M91-3	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
J14a	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
38/38	NENNADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
Clav.	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
ADP	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
SG1	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
M91-3	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
J14a	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
38/38	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
CLav.	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT

Fig. 9